

RAW SEQUENCE LISTING

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Application Serial Number: 10/021,753A
Source: 1FW16
Date Processed by STIC: 12/2/04

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IFW16

RAW SEQUENCE LISTING

DATE: 12/02/2004

PATENT APPLICATION: US/10/021,753A

TIME: 11:34:35

Input Set : D:\UTSH251US.APP.txt

Output Set: N:\CRF4\12022004\J021753A.raw

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3 <110> APPLICANT: FUJISE, KEN
4   YEH, EDWARD T.H.
6 <120> TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO FORTILIN, AN
7   ANTI-APOPTOTIC MOLECULE, AND MODULATORS OF FORTILIN
9 <130> FILE REFERENCE: UTSH:251US
11 <140> CURRENT APPLICATION NUMBER: 10/021,753A
12 <141> CURRENT FILING DATE: 2001-10-30
14 <150> PRIOR APPLICATION NUMBER: 60/244,416
15 <151> PRIOR FILING DATE: 2000-10-30
17 <160> NUMBER OF SEQ ID NOS: 9
19 <170> SOFTWARE: PatentIn Ver. 2.1
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 830
23 <212> TYPE: DNA
24 <213> ORGANISM: Homo sapiens
26 <220> FEATURE:
27 <221> NAME/KEY: CDS
28 <222> LOCATION: (95)..(613)
30 <400> SEQUENCE: 1
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32 ctagecgccgt cgctgctctcc cttcagtcgc catc atg att atc tac cgg gac ctc 115
33                                     Met Ile Ile Tyr Arg Asp Leu
34                                     1           5
37 atc agc cac gat gag atg ttc tcc gac atc tac aag atc cgg gag atc 163
38 Ile Ser His Asp Glu Met Phe Ser Asp Ile Tyr Lys Ile Arg Glu Ile
39      10           15           20
41 gcg gac ggg ttg tgc ctg gag gtg gag ggg aag atg gtc agt agg aca 211
42 Ala Asp Gly Leu Cys Leu Glu Val Glu Gly Lys Met Val Ser Arg Thr
43      25           30           35
45 gaa ggt aac att gat gac tcg ctc att ggt gga aat gcc tcc gct gaa 259
46 Glu Gly Asn Ile Asp Asp Ser Leu Ile Gly Gly Asn Ala Ser Ala Glu
47  40           45           50           55
49 ggc ccc gag ggc gaa ggt acc gaa agc aca gta atc act ggt gtc gat 307
50 Gly Pro Glu Gly Glu Gly Thr Glu Ser Thr Val Ile Thr Gly Val Asp
51      60           65           70
53 att gtc atg aac cat cac ctg cag gaa aca agt ttc aca aaa gaa gcc 355
54 Ile Val Met Asn His His Leu Gln Glu Thr Ser Phe Thr Lys Glu Ala
55      75           80           85
57 tac aag aag tac atc aaa gat tac atg aaa tca atc aaa ggg aaa ctt 403
58 Tyr Lys Lys Tyr Ile Lys Asp Tyr Met Lys Ser Ile Lys Gly Lys Leu
59      90           95          100
61 gaa gaa cag aga cca gaa aga gta aaa cct ttt atg aca ggg gct gca 451
62 Glu Glu Gln Arg Pro Glu Arg Val Lys Pro Phe Met Thr Gly Ala Ala

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63      105      110      115
65 gaa caa atc aag cac atc ctt gct aat ttc aaa aac tac cag ttc ttt 499
66 Glu Gln Ile Lys His Ile Leu Ala Asn Phe Lys Asn Tyr Gln Phe Phe
67 120      125      130      135
69 att ggt gaa aac atg aat cca gat ggc atg gtt gct cta ttg gac tac 547
70 Ile Gly Glu Asn Met Asn Pro Asp Gly Met Val Ala Leu Leu Asp Tyr
71      140      145      150
73 cgt gag gat ggt gtg acc cca tat atg att ttc ttt aag gat ggt tta 595
74 Arg Glu Asp Gly Val Thr Pro Tyr Met Ile Phe Phe Lys Asp Gly Leu
75      155      160      165
77 gaa atg gaa aaa tgt taa caaatgtggc aattattttg gatctatcac 643
78 Glu Met Glu Lys Cys
79      170
81 ctgtcatcat aactggcttc tgcttgatc ccacacaaca ccaggactta agacaaatgg 703
83 gactgatgtc atcttgagct cttcatttat tttgactgtg atttatttgg agtggaggca 763
85 ttgtttttaa gaaaaacatg tcatgtaggt tgtctaaaaa taaaatgcat ttaaaactcat 823
87 ttgagag 830
90 <210> SEQ ID NO: 2
91 <211> LENGTH: 172
92 <212> TYPE: PRT
93 <213> ORGANISM: Homo sapiens
95 <400> SEQUENCE: 2
96 Met Ile Ile Tyr Arg Asp Leu Ile Ser His Asp Glu Met Phe Ser Asp
97 1 5 10 15
98 Ile Tyr Lys Ile Arg Glu Ile Ala Asp Gly Leu Cys Leu Glu Val Glu
99 20 25 30
100 Gly Lys Met Val Ser Arg Thr Glu Gly Asn Ile Asp Asp Ser Leu Ile
101 35 40 45
102 Gly Gly Asn Ala Ser Ala Glu Gly Pro Glu Gly Glu Gly Thr Glu Ser
103 50 55 60
104 Thr Val Ile Thr Gly Val Asp Ile Val Met Asn His His Leu Gln Glu
105 65 70 75 80
106 Thr Ser Phe Thr Lys Glu Ala Tyr Lys Lys Tyr Ile Lys Asp Tyr Met
107 85 90 95
108 Lys Ser Ile Lys Gly Lys Leu Glu Glu Gln Arg Pro Glu Arg Val Lys
109 100 105 110
110 Pro Phe Met Thr Gly Ala Ala Glu Gln Ile Lys His Ile Leu Ala Asn
111 115 120 125
112 Phe Lys Asn Tyr Gln Phe Phe Ile Gly Glu Asn Met Asn Pro Asp Gly
113 130 135 140
114 Met Val Ala Leu Leu Asp Tyr Arg Glu Asp Gly Val Thr Pro Tyr Met
115 145 150 155 160
116 Ile Phe Phe Lys Asp Gly Leu Glu Met Glu Lys Cys
117 165 170
121 <210> SEQ ID NO: 3
122 <211> LENGTH: 172
123 <212> TYPE: PRT
124 <213> ORGANISM: Rabbit
126 <400> SEQUENCE: 3

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127 Met Ile Ile Tyr Arg Asp Leu Ile Ser His Asp Glu Met Phe Ser Asp
128 1 5 10 15
130 Ile Tyr Lys Ile Arg Glu Ile Ala Gly Gly Leu Cys Leu Glu Val Glu
131 20 25 30
133 Gly Lys Met Val Ser Arg Thr Glu Gly Asn Ile Asp Asp Ser Leu Ile
134 35 40 45
136 Gly Gly Asn Ala Ser Ala Glu Gly Pro Glu Gly Glu Gly Thr Glu Ser
137 50 55 60
139 Thr Val Ile Thr Gly Val Asp Ile Val Met Asn His His Leu Gln Glu
140 65 70 75 80
142 Thr Ser Phe Thr Lys Glu Ala Tyr Lys Lys Tyr Ile Lys Asp Tyr Met
143 85 90 95
145 Lys Ser Ile Lys Gly Lys Leu Glu Glu Gln Arg Pro Glu Arg Val Lys
146 100 105 110
148 Pro Phe Met Thr Gly Ala Ala Glu Gln Ile Lys His Ile Leu Ala Asn
149 115 120 125
151 Phe Lys Asn Tyr Gln Phe Tyr Ile Gly Glu Asn Met Asn Pro Asp Gly
152 130 135 140
154 Met Val Ala Leu Leu Asp Tyr Arg Glu Asp Gly Val Thr Pro Phe Met
155 145 150 155 160
157 Ile Phe Phe Lys Asp Gly Leu Glu Met Glu Lys Cys
158 165 170
161 <210> SEQ ID NO: 4
162 <211> LENGTH: 172
163 <212> TYPE: PRT
164 <213> ORGANISM: Mus musculus
166 <400> SEQUENCE: 4
167 Met Ile Ile Tyr Arg Asp Leu Ile Ser His Asp Glu Leu Phe Ser Asp
168 1 5 10 15
170 Ile Tyr Lys Ile Arg Glu Ile Ala Asp Gly Leu Cys Leu Glu Val Glu
171 20 25 30
173 Gly Lys Met Val Ser Arg Thr Glu Gly Ala Ile Asp Asp Ser Leu Ile
174 35 40 45
176 Gly Gly Asn Ala Ser Ala Glu Gly Pro Glu Gly Glu Gly Thr Glu Ser
177 50 55 60
179 Thr Val Val Thr Gly Val Asp Ile Val Met Asn His His Leu Gln Glu
180 65 70 75 80
182 Thr Ser Phe Thr Lys Glu Ala Tyr Lys Lys Tyr Ile Lys Asp Tyr Met
183 85 90 95
185 Lys Ser Leu Lys Gly Lys Leu Glu Glu Gln Lys Pro Glu Arg Val Lys
186 100 105 110
188 Pro Phe Met Thr Gly Ala Ala Glu Gln Ile Lys His Ile Leu Ala Asn
189 115 120 125
191 Phe Asn Asn Tyr Gln Phe Phe Ile Gly Glu Asn Met Asn Pro Asp Gly
192 130 135 140
194 Met Val Ala Leu Leu Asp Tyr Arg Glu Asp Gly Val Thr Pro Phe Met
195 145 150 155 160
197 Ile Phe Phe Lys Asp Gly Leu Glu Met Glu Lys Cys
198 165 170

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Input Set : D:\UTSH251US.APP.txt

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201 <210> SEQ ID NO: 5

202 <211> LENGTH: 172

203 <212> TYPE: PRT

204 <213> ORGANISM: Chicken

206 <400> SEQUENCE: 5

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207 Met Ile Ile Tyr Arg Asp Cys Ile Ser Gln Asp Glu Met Phe Ser Asp
208   1           5           10           15
210 Ile Tyr Lys Ile Arg Glu Val Ala Asn Gly Leu Cys Leu Glu Val Glu
211           20           25           30
213 Gly Lys Met Val Thr Arg Thr Glu Gly Gln Ile Asp Asp Ser Leu Ile
214           35           40           45
216 Gly Gly Asn Ala Ser Ala Glu Gly Pro Glu Gly Glu Gly Thr Glu Ala
217           50           55           60
219 Thr Val Ile Thr Gly Val Asp Ile Val Ile Asn His His Leu Gln Glu
220  65           70           75           80
222 Thr Ser Phe Thr Lys Glu Ser Tyr Lys Lys Tyr Ile Lys Asp Tyr Met
223           85           90           95
225 Lys Ala Ile Lys Ala Arg Leu Glu Glu His Lys Pro Glu Arg Val Lys
226           100          105          110
228 Pro Phe Met Thr Gly Ala Ala Glu Gln Ile Lys His Ile Leu Ala Asn
229           115          120          125
231 Phe Lys Asn Tyr Gln Phe Phe Ile Gly Glu Asn Met Asn Pro Asp Gly
232           130          135          140
234 Met Val Ala Leu Leu Asp Phe Arg Glu Asp Gly Val Thr Pro Tyr Met
235 145          150          155          160
237 Ile Phe Phe Lys Asp Gly Leu Glu Ile Glu Lys Cys
238           165          170

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241 <210> SEQ ID NO: 6

242 <211> LENGTH: 172

243 <212> TYPE: PRT

244 <213> ORGANISM: D. Melanogaster

246 <400> SEQUENCE: 6

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247 Met Lys Ile Tyr Lys Asp Ile Ile Thr Gly Asp Glu Met Phe Ala Asp
248   1           5           10           15
250 Thr Tyr Lys Met Lys Leu Val Asp Asp Val Ile Tyr Glu Val Tyr Gly
251           20           25           30
253 Lys Leu Ile Thr Arg Gln Gly Asp Asp Ile Lys Leu Glu Gly Ala Asn
254           35           40           45
256 Ala Ser Ala Glu Glu Ala Asp Glu Gly Thr Asp Ile Thr Ser Glu Ser
257           50           55           60
259 Gly Val Asp Val Val Leu Asn His Arg Leu Thr Glu Cys Phe Ala Phe
260  65           70           75           80
262 Gly Asp Lys Lys Ser Tyr Thr Leu Tyr Leu Lys Asp Tyr Met Lys Lys
263           85           90           95
265 Val Leu Ala Lys Leu Glu Glu Lys Ser Pro Asp Gln Val Asp Ile Phe
266           100          105          110
268 Lys Thr Asn Met Asn Lys Ala Met Lys Asp Ile Leu Gly Arg Phe Lys
269           115          120          125
271 Glu Leu Gln Phe Phe Thr Gly Glu Ser Met Asp Cys Asp Gly Met Val

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272      130      135      140
274 Ala Leu Val Glu Tyr Arg Glu Ile Asn Gly Asp Ser Val Pro Val Leu
275 145      150      155      160
277 Met Phe Phe Lys His Gly Leu Glu Glu Glu Lys Cys
278      165      170
281 <210> SEQ ID NO: 7
282 <211> LENGTH: 181
283 <212> TYPE: PRT
284 <213> ORGANISM: C. ELEGANS
286 <400> SEQUENCE: 7
287 Met Leu Ile Tyr Lys Asp Ile Ile Ser Asp Asp Glu Leu Ser Ser Asp
288 1      5      10      15
290 Ser Phe Pro Met Lys Leu Val Asp Asp Leu Val Tyr Glu Phe Lys Gly
291      20      25      30
293 Lys His Val Val Arg Lys Glu Gly Glu Ile Val Leu Ala Gly Ser Asn
294      35      40      45
296 Pro Ser Ala Glu Glu Gly Ala Glu Asp Asp Gly Ser Asp Glu His Val
297      50      55      60
299 Glu Arg Gly Ile Asp Ile Val Leu Asn His Lys Leu Val Glu Met Asn
300 65      70      75      80
302 Cys Tyr Glu Asp Ala Ser Met Phe Lys Ala Tyr Ile Lys Lys Phe Met
303      85      90      95
305 Lys Asn Val Ile Asp His Met Glu Lys Asn Asn Arg Asp Lys Ala Asp
306      100      105      110
308 Val Asp Ala Phe Lys Lys Lys Ile Gln Gly Trp Val Val Ser Leu Leu
309      115      120      125
311 Ala Lys Asp Arg Phe Lys Asn Leu Ala Phe Phe Ile Gly Glu Arg Ala
312      130      135      140
314 Ala Glu Gly Ala Glu Asn Gly Gln Val Ala Ile Ile Glu Tyr Arg Asp
315 145      150      155      160
317 Val Asp Gly Thr Glu Val Pro Thr Leu Met Leu Val Lys Glu Ala Ile
318      165      170      175
320 Ile Glu Glu Lys Cys
321      180
324 <210> SEQ ID NO: 8
325 <211> LENGTH: 166
326 <212> TYPE: PRT
327 <213> ORGANISM: S. Cerevisiae
329 <400> SEQUENCE: 8
330 Met Ile Ile Tyr Lys Asp Ile Phe Ser Asn Asp Glu Leu Leu Ser Asp
331 1      5      10      15
333 Ala Tyr Asp Ala Lys Leu Val Asp Asp Val Ile Tyr Glu Ala Asp Cys
334      20      25      30
336 Ala Met Val Asn Val Gly Gly Asp Asn Ile Asp Ile Gly Ala Asn Pro
337      35      40      45
339 Ser Ala Glu Gly Gly Asp Asp Asp Val Glu Glu Gly Ala Glu Met Val
340      50      55      60
342 Asn Asn Val Val His Ser Phe Arg Leu Gln Gln Thr Ala Phe Asp Lys
343 65      70      75      80

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VERIFICATION SUMMARY

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Input Set : D:\UTSH251US.APP.txt

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